

AMENDMENTS TO THE SPECIFICATION

Please amend the Brief Description of the Drawings beginning on page 6, line 22, as follows:

--Brief Description of Drawings

FIG. 1 shows the mugineic acids' biosynthesis route for a barley root with an iron deficiency and its rhizospheric environment.

FIG. 2 shows the genetic sequence of the binary vector pIG121Hm for a gramineae transformation in which the cDNA of *naat-A* is inserted.

FIG. 3 is a photo in place of a drawing that shows the results when detection of the introduced gene is carried out by the Southern Hybridization method. WT in FIG. 3 shows a case of an autochthon gramineae, and the control shows a control gramineae in which only the vector was introduced. 1-5, 1-6, 1-7, 8-1 and 15-2 show transformants having a 35S promoter.

FIG. 4 shows the result of measurement of NAAT activity in a root cultivated in a hydroponic solution in the presence of iron (+Fe) and an iron deficiency (-Fe). In FIG. 4, the whited out portion shows the case for +Fe and the shaded portion shows the case of -Fe. WT shows an autochthon type and 1-5, 1-6 and 1-7 show transformants.

FIG. 5 is a photo in place of a drawing that shows the growing state of each gramineae which is 8 weeks after a transplanting to alkaline soil. The control in FIG. 5 shows the control gramineae in which only the vector is transplanted and the gramineae on the right is the one that is transformed.

FIG. 6 is a graph that shows a transition of the height of each gramineae after being transplanted to alkaline soil. A black dot shows the transformer 15-2, a black square shows the transformer 8-1, and a white dot shows the control gramineae in which only the vector was transplanted.

FIG. 7 shows a limited enzyme map of a phage DNA including an isolated genome *naat*. In FIG. 7, E indicates *EcoRI*, H indicates *HindIII*, B indicates *BamHI*, and N indicates *NotI*. The *NotI* site on both sides is the *NotI* located at the arm of λ FIXII.

FIG. 8 shows the genetic sequence of the binary vector pBIGRZ1 for a transformed gramineae in which a fragment of the NAAT genome is inserted. In FIG. 8, NPTII is a kanamycin resistant gene, HPT is a hygromycin resistant gene, GUS is a β glucuronidase gene with intron, LacZ is a β galactosidase gene, 35P is a 35S promoter, NP is an NOS promoter, NT

is an NOS terminator, MCS is a multi-cloning site, and Riori is an Ri plasmid replication starting point.

FIGS. 9A through 9D is a drawing showing show the base sequence (SEQ. ID No. 3) of the obtained genome *naat*.

FIGS. 10A through 10G is a drawing that shows the base sequence of *naat* (SEQ. ID No. 3) and 5' upstream of *naat-A* and *naat*, the exon, the intron and 3' downstream, which were determined by comparing with the cDNA. In FIGS. 10A through 10G, the uppercase letters show the exon portion that is a transcription on the cDNA (SEQ. ID No. 1 and 2) and the lowercase letters show the rest.

FIG. 11 is a schematic view of the obtained genome fragment. In FIG. 11, E is *EcoRI*, H is *HindIII* and B is *BamHI*.

FIG. 12 shows the size of the intron in the cDNA of *naat-A* and *naat*.

FIG. 13 shows an amino acid expressed in a single letter code of an amino acid sequence of NAAT-A (SEQ. ID No. 1) estimated from the cDNA.

FIG. 14 shows an amino acid expressed in a single letter code of an amino acid sequence of NAAT-B (SEQ. ID No. 2) estimated from the cDNA.

FIGS. 15A and 15B are photographs in place of drawings that shows the growing state of each gramineae, ten (10) weeks after being transplanting to an alkaline soil. The control in FIGS. 15A and 15B shows the control gramineae in which only the vector is transplanted and the gramineae on the right is the one that is transformed with a genome *naat*.

FIG. 16 is a graph that shows the transition of the height of each gramineae in which a genome *naat* was introduced after being transplanted to alkaline soil. In FIG. 16, the gramineae on the left is the one transformed with *naat* and the one on the right is the control gramineae in which only the vector was transplanted.--

Please amend the paragraph beginning on page 14, line 11, as follows:

--Sequence Identification No. 4 3 in the sequence table listing shows the determined 10,966 10,966 bp base sequence. In addition, the entire sequence is shown in FIGS. 9A through 9D (without base number).

Please amend the paragraph beginning on page 25, line 9, as follows:

--Primers for fragment A

Name: Sequence F-A1F: FITC-5'-gct act agt agt att cct ggt gta g (SEQ. ID No. 4)

Name: Sequence F-A1R: FITC-5'-gga gta cta cta gac tac acc agg a (SEQ. ID No. 5)

Name: Sequence F-A2F: FITC-5'-aca tgc gca tgc atg aat tgc cg (SEQ. ID No. 6)

Name: Sequence F-A2R: FITC-5'-caa ttc atg cat gcg cat gtg cc (SEQ. ID No. 7)--.

Please amend the paragraph beginning on page 25, line 14, as follows:

--Primers for fragment B

Name: Sequence F-B1F: FITC-5'-ggg caa gta tgc agt atg ttg gaa c (SEQ. ID No. 8)

Name: Sequence F-B1R: FITC-5'-gtt cca aca tac tgc ata ctt gac c (SEQ. ID No. 9)

Name: Sequence F-B2F: FITC-5'-cta gaa gcc tat gga tgt ttc ttt tgg (SEQ. ID No. 10)

Name: Sequence F-B2R: FITC-5'-cca aaa gaa aca tcc ata ggc ttc tag (SEQ. ID No. 11)

Name: Sequence F-B3F: FITC-5'-agt tct tat caa ttt ccg aga tga c (SEQ. ID No. 12)

Name: Sequence F-B3R: FITC-5'-ata gtc atc tcg gaa att gat aag a (SEQ. ID No. 13)

Name: Sequence F-B4F: FITC-5'-agt ggt cac cat gcg gac caa cac c (SEQ. ID No. 14)

Name: Sequence F-B4R: FITC-5'-ggg gtt ggt ccg cat ggt gac cac t (SEQ. ID No. 15)--.

Please amend the paragraph beginning on page 25, line 23 as follows:

--Primers for fragment C

Name: Sequence F-C1F: FITC-5'-cac cgg cca gtt caa ctg cta cgc (SEQ. ID No. 16)

Name: Sequence F-C1R: FITC-5'-gcg tag cag ttg aac tgg ccg gtg (SEQ. ID No. 17)

Name: Sequence F-C2F: FITC-5'-ttt gga gga gat cca tga cga cat a (SEQ. ID No. 18)

Name: Sequence F-C2R: FITC-5'-tat gtc gtc atg gat ctc ctc caa a (SEQ. ID No. 19)

Name: Sequence F-C3F: FITC-5'-tct tct cat atg cta ctg tgg gga t (SEQ. ID No. 20)

Name: Sequence F-C3R: FITC-5'-tga cat gca aca cag gga cat gag c (SEQ. ID No. 21)--.

Please amend the paragraph beginning on page 26, line 7, as follows:

--Primers for fragment D

Name: Sequence F-D1F: FITC-5'-cat gct gac gaa gag cga ggt cat a (SEQ. ID No. 22)

Name: Sequence F-D1R: FITC-5'-ccc agg ata tga cct tag tgg ttg g (SEQ. ID No. 23)--.

Please amend the paragraph beginning on page 26, line 13, as follows:

--Primers for fragment B

Name: Sequence B5F: 5'-gaa tgg caa act ggg tcc gca tta c (SEQ. ID No. 24)
Name: Sequence B5R: 5'-gta atg cgg acc cag ttt gcc att c (SEQ. ID No. 25)
Name: Sequence B6F: 5'-ctg gtt gtt gtg gcc tgg acg aaa c (SEQ. ID No. 26)
Name: Sequence B6R: 5'-gtt tcg tcc agg cca caa caa cca g (SEQ. ID No. 27)
Name: Sequence B7F: 5'-agc aca aac cct acc tat gtt agg c (SEQ. ID No. 28)
Name: Sequence B7R: 5'-gcc taa cat agg tag ggt ttg tgc t (SEQ. ID No. 29)--.

Please amend the paragraph beginning on page 26, line 20, as follows:

--Primers for fragment C

Name: Sequence C4F: 5'-tgg aat ttc gcc cgg ggc aag gac (SEQ. ID No. 30)
Name: Sequence C4R: 5'-ccc tgt gac aag tgc tct gct acg (SEQ. ID No. 31)
Name: Sequence C5F: 5'-tct ggg atc tca gtg cat cca aca (SEQ. ID No. 32)
Name: Sequence C5R: 5'-gaa gca tat atc agt caa aca taa cc (SEQ. ID No. 33)--.

Please amend the paragraph beginning on page 27, line 6, as follows:

--Border between fragments A and B

Name: Sequence A-eF: 5'-cac atc ctt tgc ctt gct gaa tat gg (SEQ. ID No. 34)
Name: Sequence B-tR: 5'-cag tag tac taa tta atc acc tta gta gc (SEQ. ID No. 35)--.

Please amend the paragraph beginning on page 27, line 10, as follows:

--Border between fragments B and C

Name: Sequence B-eF: 5'-cac gat caa cca aag aat gtc ctc c (SEQ. ID No. 36)
Name: Sequence C-tR: 5'-tac ttg tat atg cag ctc cag cac (SEQ. ID No. 37)--.

Please amend the paragraph beginning on page 27, line 13, as follows:

--(7) The sequence identification number ~~1~~ 3 in the sequence listing of the determined 10,966 bp base sequence is shown. The entire sequence is shown in FIGS. 9A through 9D (without base number).